# SEQUENCE LISTING

(1)		GENERAL INFORMATION	
(1)	(I)		
	(i)	APPLICANTS:	A 1 17 1 1 1 Count did a Vincia d
		(A) NAME:	Advanced Technologies (Cambridge) Limited
		(B) STREET:	Globe House, 1 Water Street
		(C) CITY:	London
		(E) COUNTRY:	England /
		(F) POSTAL CODE:	WC2R 3LA
		• •	
	(ii)	TITLE OF INVENTION:	Modification of Plant Fibres
	` '		
	(iii)	NUMBER OF SEQUENCES:	8
	(22)		- /
	(iv)	CORRESPONDENCE ADDRESS:	
	()	(A) ADDRESSEE:	British American Tobacco (Investments) Limited
		(B) STREET:	Regents Park Road
		(C) CITY: /	Southampton
		(D) STATE:	Hampshire
		(E) COUNTRY:	England
		(F) POSTAL CODE:	SO15 8TL
		(1) TOSTAL CODE.	5013 012
	(v)	COMPUTER READABLE FORM:	)
	(•)	(A) MEDIUM TYPE:	Diskette 3.50 inch
		(B) COMPUTER:	Viglen P5/75
		(C) OPERATING SYSTEM: V	MS-DOS Windows 95
		(D) SOFTWARE:	Microsoft Word 97
		(D) SOFTWARE.	Wheresoft Word 27
	(vi)	CURRENT APPLICATION DATA:	
	(**)	(A) APPLICATION NUMBER:	Not yet known
		(C) CLASSIFICATION:	Not yet known
		(C) CLABBILICATION.	Not yet known
	(viii)	ATTORNEY/AGENT	
	()	INFORMATION:	,
		(A) NAME:	Mrs. M.R. Walford/ Mr. K.J.H. MacLean
		(C) REFERENCE:	RD-ATC-19
		(6) 1212/21(62)	
	(ix)	TELECOMMUNICATION	
	()	INFORMATION:	
		(A) TELEPHONE:	01703 777155
		(B) /TELEFAX:	01703 779856
		(b) JELLIAA.	01/05/1/050
		/	
		/	
		/	
		/	
		/	

## INFORMATION FOR SEQ.ID. NO:1 (2)

SEQUENCE CHARACTERISTICS (i)

(A)	LENGTH:	488 bps
(B)	TYPE:	Nucleic acid
(C)	STRANDEDNESS:	Double
(D)	TOPOLOGY:	J∠inear

(D) TOPOLOGY:

cDNA

### **MOLECULE TYPE:** (ii)

#### ORIGINAL SOURCE: (vi)

(A) ORGANISM:

Eucalyptus grandis

#### SEQUENCE DESCRIPTION: (xi)

SEQ. ID. NO:1:

I X	
ATGGGGGGG CTTGTGGGTA TGGCACGTG TACAGCCAAG GCTATGGCAC	50
CAACACIGCA GCTTIGAGCA CIGCOCIGTT CAACAATGGC CIGAGCIGCG	100
COCCATCITA CCACATCCCC TCCAACCACC ACCCCACGIG GTCCCTCCCC	150
GOGACCATCA TOGTCACOGC AACCAACTTT TGCCCTCCCA ACTTGGCCCT	200
CTCCAACGAC AATTGCGGCT GGTGCAACCC CCCTCTCCAG CACTTCGATA	250
TGGCCGAGCC TGCTTTCTTG CAGATTGCCC AGTACAAAGC TGGGATTGTC	300
CAGGITICCT TCAGAAGGT TCCGIGIGIG AAGAAAGGAG GGGIAAGGIT	350
CACCATCAAT GOCCACTCCT ACTTCAACTT GGTGCTGATC ACCAACGTGG	400
CACCICCICC TCATCICCAT TCCGITTCCA TCAACCCCIC GACGACICCI	450
TGGCAAGCCA TGTCAAGGAA CTGGGGCAAA AACTGGCA	488

(2)	(i)	INFORMATION FOR SEQ. ID. NO:2 SEQUENCE CHARACTERISTICS:	
	(-)	(A) LENGTH:	475 base pairs
		(B) TYPE:	Nucleic acid
		(C) STRANDEDNESS:	Double/
		(D) TOPOLOGY:	Linear
	(ii)	MOLECULE TYPE:	cDNA
	(vi)	ORIGINAL SOURCE: (A) ORGANISM:	Eucalyptus grandis

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO:2:

ATGGGGGGG CATGGGGTA TGGCAACCTG TACAGCCAAG GCTATGGCAC	50
CAACACTGCA GCTTTGAGCA CTGCCCTGTT CAACAATGGC CTGAGCTGCG	. 100
GOCCATGITA CCAGATCCGG TCCAACCACG ACCCCAGGIG GTCCCICCCG	150
GGCACCATCA TGGTCACGGC AACCAACTTT TGCCCTCCCA ACTTGCCCCT	200
CTCCAACGAC AATGGCGCT GGTGCAACCC CCCTCTCCAG CACTTCGATA	250
TOCCOGAGOC TOCCTTCTTG CAGATTOCCC AGTACAAAGC TOCCATTGTC	. 300
CCCGTTTCCT TCAGAACGCT TCCGTGTGTG AAGAAAGCAG GCGTAACGTT	350
CACCATCAAT GEGCACICCT ACTTCAGCIG TEGTGCTGAT CACCAACGIG	400
GCAGGIGCIV GIGATGICCA TICCGITTCC ATCAAGAGCT CGAGGACIGG	450
TIGGCAAGCC AIGICAAGGA AIIGA	475

(2) (i)	INFORMATION FOR SEQ. ID SEQUENCE CHARACTERIST (A) LENGTH: (B) TYPE: (C) STRANDEDNESS: (D) TOPOLOGY:		<i></i>
(ii)	MOLECULE TYPE:	cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM:	Euclayptus gran	ıdis
(xi)	SEQUENCE DESCRIPTION:	SEQ. ID. NO:3:	
ATGGGGGG	OC CATCICCITA CCCCCACCIZ CA	CAGGGCCA CCIATGGCAA	50
GIACAGIG	CC CCCTICACCT CCATCCTCTT CA	ACAGAGGG AGIACCIGCG	100
GGGCTTGC	TT CGACCTCCCC TCCCTCCACC AC	ATTTIGIG GIGCCICCCT	150
GGTAGCCC	ET COGTGATCCT CACCCCCACC GA	CTTCTGCC CTCCCAACTA	200
cecectice	CC CCACATIACC CCCCCICCIC CA	ACTICCOG CACGAGCACT	250
TCGAGATG	TIC GCAGGCCGCC TICGCCGAGA TI	GOOGTOOG AAGOOCTGAT	300
GIGGIGCC	TA TCCACTACAG GAGGGTGAAC TG	TCTGAGAA GCCGTCGTCT	350

GAGATICACA TIGAGCOGAA ACTCICACTI CITICAGGIC TIGGIGACGA

ATGTAGGCCT/AGATGGGGAG GTGATTGCCA TGAAAATGAA GGGATCGAAA

ACACCGIGCA TACCGATCGC AAGAAACTCG GGCAAAAACT GGCA

450

494

## **INFORMATION FOR SEQ. ID. NO:4 (2) SEQUENCE CHARACTERISTICS:** (i) (A) LENGTH: 437 base pairs Nucleic acid (B) TYPE Double (C) STRANDEDNESS: (D) TOPOLOGY: Linear çĎNA **MOLECULE TYPE:** (ii) (vi) **ORIGINAL SOURCE:** Eucalyptus grandis (A) ORGANISM: SEQUENCE DESCRIPTION: SEQ. ID. No. 4 (xi) ATGGGTTGCC ACCGGGTCCT TGATCCTPTG ATGGCCACGG AGTGCACATC 50 CCCTGCTCCG CCGACATTGG TTATYAGCAC GAGGITGAAA TAAGAATGGC 100 CGITGACGGT GAACCGGATC CXTCCGCTTC TCCTGCACCT CACTCTTCGG 150 200 TAGGCCACCG GGACGATCCC GGCCCTGTAC TGCGCAATGT GCTGGAAGAC CGCCTGGGAG AGGTCGAAAT GGAGTTGAGG AGGGTCGCAC CACCCTCCTG 250 GAGGCCAGAA GITOGTCGCC GTGACCACAA TGGCGCCCGG GAGGCACCAC 300

TGCGGGTCGT TCACGCACCG GAGCTCAAAG CACGCGCCGC AGCTCAGCCC

ATTGTTGAAC AATGCAGTGC TCAGTGCAGC TGTGTTTGTG CCGTACCCTT

GCTGTATAG ATTCCCATAA CCACACGCCC CCCCCAT

350

400

437

## **INFORMATION FOR SEQ. ID. NO:5 (2) SEQUENCE CHARACTERISTICS: (i)** 437 base pairs (A) LENGTH: (B) TYPE Nucleic acid Doyble (C) STRANDEDNESS: (D) TOPOLOGY: Linear cDNA (ii) **MOLECULE TYPE: ORIGINAL SOURCE:** (vi) (A) ORGANISM: Eucalyptus grandis SEQUENCE DESCRIPTIÓN SEQ. ID. No. 5 (xi) ATGGGTTGCC ACCGGGTCCT TGATACTTTG ATGGCCACGG AGTGCACATC 50 CCCTCCTCCG CCGACATTGG TATCACCAC GAGGITGAAA TAAGAATGCC 100 CGTTGACGGT GAACCGGATIĆ CCTCCGCTTC TCCTGCACCT CACTCTTCGG 150 TAGGCCACAG GGACGATCCC GGCCCTGTAC TGCGCAATGT GCTGGAAGAC 200 AGGCTGGGAG AGGTCGAAAT GGAGTTGAGG AGGGTCGCAC CACCCTCCTG 250 GAGGCAGAA OTTGGTOGCC GTGACAACAA TGGCGCCCGG GAGGCACCAC 300

TGCGGGTCGT TCACGCACCG GAGCTCAAAG CACGCGCCGC AGCTCAGCCC

ATTGITGÁAC AATGCAGTGC TCAGTGCAGC TGTGITTGTG CCGTACCCTT

GCCTOTATAG ATTOCCATAA CCACACGCCC CCCCCAT

350

400

437

## **(2) INFORMATION FOR SEQ. ID. NO:6** SEQUENCE CHARACTERISTICS: **(i)** (A) LENGTH: 488 base pairs Nucleic acid (B) TYPE (C) STRANDEDNESS: Double (D) TOPOLOGY: Linear cØNA (ii) **MOLECULE TYPE: ORIGINAL SOURCE:** (vi) Eucalyptus grandis (A) ORGANISM: SEQUENCE DESCRIPTION: SEQ. ID. No. 6 (xi)

CCTTGACATG GTCTGCCACC TTGTCCGCCA ACCCTTCACG GCCACCGAGT	50
TGACGITGCC TGCGCCGCCG ACGITTGTGA CGAGGACGAG CTTGAAGIAT	100
CACTICCCCT TCATCCTCAA COCCATCCCT CCTCTCCTCC TCCACCTCAC	150
CCTCCTGTAC GCAACGTGGA CGATGCCGGC TCGGTACTTG GCAATGTGCT	200
GCAAGACGGG CTGCGAGATG TCGAAGTGGT GTTGCGCGCGG GTTGCACCAT	250
CCCCCCCCCT TCTTTCCCAG CCCCTTCTTT CCCCCCCACA ACTTTCTCCC	300
GCTGACGACG ATGCAGCCGC CCAGGCACCA CTTTCCGTCG TTCACGCACC	350
GCATCTCCAA CCACGACCCC CACCTCAGCC CCTTTTTTAA CAGCCCCGTG	400
CTCAGCGCGG CCGTGTTCGT ACCGTAGCCC TGGCTGTACA GGTTGCCG	448

#### **INFORMATION FOR SEQ. ID. NO:7 (2)** ·

- **SEQUENCE CHARACTERISTICS: (i)** 
  - (A) LENGTH:
  - (B) TYPE
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY:

19 nucleotides

Nucleic acid

Single

Linear

- **MOLECULE TYPE:** (ii)

**SEQUENCE DESCRIPTION:** 

SEQ. ID. No. 7

Synthetic DNA

ATGGIGGIGC NIGIGGNIA

(xi)

19

Key Inosine Ι

A, G, T, or C

INFORMATION FOR SEQ. ID. NO:8 **(2)** 

- SEQUENCE CHARACTERISTICS: **(i)** 
  - (A) LENGTH:
  - (B) TYPE
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY:

- 20 nucleotides
- Nucleic acid
- Single
- Linear

**MOLECULE TYPE:** (ii)

Synthetic DNA

SEQUENCE DESCRIPTION: (xi)

SEQ. ID. No. 8

TGCCARTTYT GNCCCCARTT

20

Key = A or GR

$$Y = T \text{ or } C$$

N = A, G, T or C